

● PRINTER RUSH ●

(PTO ASSISTANCE)

Application : 09/744167

Examiner : Borin

GAU : 1631

From : PAP

Location : (IDC) FMF FDC

Date : 7/11/05

Tracking # : 06041103

Week Date : 11/15/04

DOC CODE	DOC DATE	MISCELLANEOUS
<input type="checkbox"/> 1449	_____	<input type="checkbox"/> Continuing Data
<input type="checkbox"/> IDS	_____	<input type="checkbox"/> Foreign Priority
<input type="checkbox"/> CLM	_____	<input type="checkbox"/> Document Legibility
<input type="checkbox"/> IIFW	_____	<input type="checkbox"/> Fees
<input type="checkbox"/> SRFW	_____	<input checked="" type="checkbox"/> Other <u>LET</u>
<input type="checkbox"/> DRW	_____	<u>9/20/2001</u>
<input type="checkbox"/> OATH	_____	
<input type="checkbox"/> 312	_____	
<input checked="" type="checkbox"/> SPEC	_____	

[RUSH] MESSAGE: Tables 9 + 10 are very difficult to read. Please send a better copy.

Thank you.

[XRUSH] RESPONSE: _____

corrected

See Attachment

INITIALS: 18

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.

REV 10/04

TABLE 9

NSARA	MDENMAVEDDQIKRNYSWDDQSAVENDEKCGKACLPDEKNVLVVAVMNKCCKRTQNDLQDQNNMNSDGLK	7
XSARA	WPKMVKDQIMAEQSLFNMTGSPSEIVENPSVYESD...SGLALDDQ...VNIHMKSVLLADGFSPPSSSP...KBIIN	70
NSARA	AFSLDQENROTOOFSFSINESTEKDMWSEKOMP LHPKTEKASVNMKCPSSSLASVCSFSDLKDDGSIGRDPMS	157
XSARA	FDCLTMDN...EMPLHNGMSYDNDKI...ETVTISVLPITIIQTSNVSTDPAINKP...CTKEPNR	127
NSARA	AITSITVDVSISSDGTGCPAVKKDEQYITDEDLTGKISSPRDQCEPNSFMSSEGILMKKEPAEESTTETLSRSLP	236
XSARA	ALKETTSVILPEIKPYSYCAALS FENNKNVPSYOLN...NTDULE...VSPVVEACSEIQDOKNTSBLNEEKLFEDVS	100
NSARA	LLKPDMPNGSGRMNDQCERSCDCLVPNEVRADENEGYEHELYCTEFLNTERFSESQDQTHWKTNLNEHDSOYREE	316
XSARA	ATES...FATAAEITVLOHEALSAETFDIVVKMFSDSCV...DGLTKSCGLS...QES	250
NSARA	KERFLOISQEDTNGDSQDCVGLADAGLDKCTCTSESECPSTVIOTPAANYLSNGCDSYGMDDPGVSFVFKTLPSR	396
XSARA	NEKFCASKEPE...QD...VDANVLLENACVAYKEAILPEENGTHAPMSLYNGCDSYGMKNPIAVALONPKNEPEK	310
NSARA	EDSVTEEKEIEESKSECYSNIEQDROMEARDESLLLNSTGLMKNMYLHNFSDVPSVLQDSBPKNVASLPESVFPQ	475
XSARA	EDSVTEEKEIEESKSEYTGVEEQDREDOYTERGOLLNAKADONKNNLHSLCNOVPSMHQDTSPKKGIQDLSVPPQ	388
NSARA	GARPQPSNKLQIPKPLEOMLQNDFFANSONHTKNKNDLGKAKLENSATHVCSPSLGNISNVDINGEMLESFEAE	553
XSARA	GARKOPTHLKLNPKPLETEMLQSDLIIPNACCSMYKNOMLNKSNODDLISLSLREDSAVRSPVTDANGDFFGEYRGP	478
NSARA	ISTRPCLALAPSDPNDLRAQOGTISARKPETTLGEVAPVVPDSDAPNCKMCEARFTFKRRHHCRCAGKVFCAACCSL	633
XSARA	GS...LCLAVSPDSDPNDLRAQOGFVPISKPFITTLGEVAPVVPDSDAPNCKMCEARFTFKRRHHCRCAGKVFCAACCSL	556
NSARA	KCKLQMDKKEARVCVICHSVLMNAQAWENMMSASDSPNPNNAEYCSYPPDQAQASGALSPPPTVMVYVGVKMP	713
XSARA	KCKLQMDKKEARVCVICHSEVLMNAQAWENMLASDSPNPNNAEYCSYPPDQAQASGALSPPPTVMVYVGVKMP	636
NSARA	GAEVAPRQORRVWFADQLPNGENADAIAKLTNNGTSSAGTLAYRDPVKPVITPPLAETDIFLFGSITTOVQSPYGEA	703
XSARA	DTESQSKORRVWFADGGLPNGETADSD...HAMVITVAGTLVSHNHNSTSESE...ENTSGCGSTTOVQ...EA	705
NSARA	MNLIPEQGLPPILISTGVKQDYAVEEKPQIEVMQGLEEQGDPDLPVFLNANLLSMYKIVNYVNRKCWCFTTKGMHVGQ	873
XSARA	MNLIPEQGLPPILISTGVKQDYAVEERPQIEVMQGLEEQGDPDLPVFLNANLLSMYKIVNYVNRKCWCFTTKGMHVGQ	785
NSARA	SEIVILLQCLPDEKCLPKDTNMFVQLYADALAGNVVSLNQHSEFESFLGSKHGGFLYVTSYQSLQDLVLPAPYPL	953
XSARA	AEIVILLQCLPDEKCLPKDLSMFVELYQEAIAQNVVGLNQHSEFESFLGSKHGGFLYVAPYQSLQDLVLPAPYPL	845
NSARA	DILIQKWEIPWAKVFPFRLMLRLGAEYRLYPCPLFSVRFKPLFGETQHTLMNLLADFRNYQYTLPVVQGLVQDMEVRKT	1033
XSARA	DILIQKWEIPWAKVFPFRLMLRLGAEYRLYPCPLFSVRYRKPLFGETQHTLMNLLADFRNYQYTLPVVQGLVQDMEVRKT	945
NSARA	SIKIPSNRYNEMMKAMNKSNEHVLADACFNEKADSHLVCVQNDQNYOTQAIStHNDPRKYTGASFFVFSGALKSSQY	1113
XSARA	SIKIPSNRYNEMMKAMNKSNEHVLADACFNEKADSHLVCVQNDQNYOTQAIStHNDPRKYTGASFFVFSGALKSSQY	1025
NSARA	LAKSEIVEDGVVQITAEIMDSLRQALREMKOFTITCQKADAEEDENHIDWVEDDKNYSKQVVSPIQKSMETITINVR	1193
XSARA	LAKSEIVEDGVVQITAEISMDALROSLEMKOFTITCQKADAEESDENHIDWVEDDKNIFNKGVIKSPIQKSMESVTSVR	1105
NSARA	IFHQSEYKAKQVYRWTEVFFLENDQDQNCLEDPAHNSRLTENVAKAFCLALCPNLKLLKEDGMTRGLRLVSLSDQVGY	1273
XSARA	IFHQSEYKASQKISRWTEVFFLENDQDQNCLEDPAHNSRLTENVAKAFCLALCPNLKLLKEDGMTRGLRLVSLSDQVGY	1185
NSARA	DAGENGQPLPSOYMHOLDLALVPKIHQGAQOLEEQPVVMEIIFYILENIN	1323
XSARA	DAGENGQLPARYMHOLDLALVPVHQTEQLEEQPVVMEIIFYILENIN	1235

TABLE 10

NSARA	587	GEVAPVVPDSDAPNCKMCEARFTFKRRHHCRCAGKVFCAACCSILKCKLDYMONK	655
XSARA	510	LGEVAPVVPDSDAPNCKMCEARFTFKRRHHCRCAGKVFCAACCSILKCKLDYMONK	578
KIAA0305	737	LGOKDPTVWVPEAPNCKMCEARFTFKRRHHCRCAGKVFCAACCSILKCKLDYMONK	800
FGD1	720	LGRHAPTPIREKENFDCMRCOLEPFTFKRRHHCRCAGKVFCAACCSILKCKLDYMONK	485
Hrb	153	AAERAPDWD...AEEDHRCVDFGNVTRKHHCRACGQIFCGKSSKNTBTPKFGIEKEVRCPEPYEOL	219
Hrb-2	153	AAERAPDWD...AEEDHRCVDFGNVTRKHHCRACGQIFCGKSSKNTBTPKFGIEKEVRCPEPYEOL	219
EEA4	1341	TOALNRKMEEDENONCMAEGKSEVTVRRHHCRCAGKVFCAACCSILKCKLDYMONK	1408

CONSENSUS...P-W...C-C...F...RKHORAGG-VFG-CG...RVC-C...L

SUBSTITUTE SHEET (RULE 26)